



**RAW SEQUENCE LISTING**  
**ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/840 669  
Source: O I P E  
Date Processed by STIC: 08/27/2001

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

**Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 09/840,669

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos  
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length  
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering  
The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII  
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length.  
Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"  
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)  
Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)  
Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9      Use of n's or Xaa's  
    (NEW RULES)  
Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10      Invalid <213>  
    Response  
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11    Use of <220>  
Sequence(s)    missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"  
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of n  
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH - Biotechnology Systems Branch - 08/21/2001

may  
The type of errors shown exist throughout  
the Sequence Listing. Please check subsequent  
sequences for similar errors.

OIPE

## RAW SEQUENCE LISTING

DATE: 08/27/2001

PATENT APPLICATION: US/09/840,669

TIME: 15:10:37

Input Set : A:\A-690.ST25.txt

Output Set: N:\CRF3\08272001\I840669.raw

3 <110> APPLICANT: KOHNO, TADAHIKO  
 5 <120> TITLE OF INVENTION: APO-AI/AII PEPTIDE DERIVATIVES  
 7 <130> FILE REFERENCE: A-690  
 9 <140> CURRENT APPLICATION NUMBER: 09/840,669  
 10 <141> CURRENT FILING DATE: 2001-04-23  
 12 <150> PRIOR APPLICATION NUMBER: 60/198,920  
 13 <151> PRIOR FILING DATE: 2000-04-21  
 15 <160> NUMBER OF SEQ ID NOS: 11  
 17 <170> SOFTWARE: PatentIn version 3.1  
 19 <210> SEQ ID NO: 1  
 20 <211> LENGTH: 684  
 21 <212> TYPE: DNA  
 22 <213> ORGANISM: Homo sapiens  
 24 <220> FEATURE:  
 25 <221> NAME/KEY: CDS  
 26 <222> LOCATION: (1)..(684)  
 27 <223> OTHER INFORMATION:  
 30 <400> SEQUENCE: 1  
 31 atg gac aaa act cac aca tgt cca cct tgt cca gct ccg gaa ctc ctg 48  
 32 Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu  
 33 1 5 10 15  
 35 ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc 96  
 36 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu  
 37 20 25 30  
 39 atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc 144  
 40 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser  
 41 35 40 45  
 43 cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag 192  
 44 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu  
 45 50 55 60  
 47 gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg 240  
 48 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr  
 49 65 70 75 80  
 51 tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat 288  
 52 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn  
 53 85 90 95  
 55 ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc 336  
 56 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro  
 57 100 105 110  
 59 atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag 384  
 60 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln  
 61 115 120 125  
 63 gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc 432  
 64 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val  
 65 130 135 140  
 67 agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg 480  
 68 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val

Does Not Comply  
 Corrected Diskette Needed  
*See page 3 of 7*

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Input Set : A:\A-690.ST25.txt

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```

69 145          150          155          160
71 gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct      528
72 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
73          165          170          175
75 ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc      576
76 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
77          180          185          190
79 gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg      624
80 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
81          195          200          205
83 atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg      672
84 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
85          210          215          220
87 tct ccg ggt aaa      684
88 Ser Pro Gly Lys
89 225
92 <210> SEQ ID NO: 2
93 <211> LENGTH: 228
94 <212> TYPE: PRT
95 <213> ORGANISM: Homo sapiens
97 <400> SEQUENCE: 2
99 Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
100 1          5          10          15
103 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
104          20          25          30
107 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
108          35          40          45
111 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
112          50          55          60
115 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
116 65          70          75          80
119 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
120          85          90          95
123 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
124          100          105          110
127 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
128          115          120          125
131 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
132          130          135          140
135 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
136 145          150          155          160
139 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
140          165          170          175
143 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
144          180          185          190
147 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
148          195          200          205
151 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
152          210          215          220

```

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DATE: 08/27/2001

TIME: 15:10:37

Input Set : A:\A-690.ST25.txt

Output Set: N:\CRF3\08272001\I840669.raw

155 Ser Pro Gly Lys  
 156 225  
 159 <210> SEQ ID NO: 3  
 160 <211> LENGTH: 8  
 161 <212> TYPE: PRT  
 162 <213> ORGANISM: Artificial Sequence  
 164 <220> FEATURE:  
 165 <223> OTHER INFORMATION: Preferred linker *OK*  
 167 <400> SEQUENCE: 3  
 169 Gly Gly Gly Lys Gly Gly Gly  
 170 1 5  
 173 <210> SEQ ID NO: 4  
 174 <211> LENGTH: 7  
 175 <212> TYPE: PRT  
 176 <213> ORGANISM: Artificial Sequence  
 178 <220> FEATURE:  
 179 <223> OTHER INFORMATION: Preferred linker *OK*  
 181 <400> SEQUENCE: 4  
 183 Gly Gly Asn Gly Ser Gly Gly  
 184 1 5  
 187 <210> SEQ ID NO: 5  
 188 <211> LENGTH: 8  
 189 <212> TYPE: PRT  
 190 <213> ORGANISM: Artificial Sequence  
 192 <220> FEATURE:  
 193 <223> OTHER INFORMATION: Preferred linker *OK*  
 195 <400> SEQUENCE: 5  
 197 Gly Gly Gly Cys Gly Gly Gly  
 198 1 5  
 201 <210> SEQ ID NO: 6  
 202 <211> LENGTH: 5  
 203 <212> TYPE: PRT  
 204 <213> ORGANISM: Artificial Sequence  
 206 <220> FEATURE:  
 207 <223> OTHER INFORMATION: Preferred linker ✓  
 209 <400> SEQUENCE: 6  
 211 Gly Pro Asn Gly Gly  
 212 1 5  
 215 <210> SEQ ID NO: 7  
 216 <211> LENGTH: 18  
 217 <212> TYPE: PRT  
 218 <213> ORGANISM: Artificial Sequence  
 220 <220> FEATURE:  
 221 <223> OTHER INFORMATION: Peptide *Errored*  
 223 <400> SEQUENCE: 7  
 225 Asp Trp Leu Lys Ala Phe Tyr Asp Lys Val Ala Glu Lys Leu Lys Glu  
 226 1 5 10 15  
 229 Ala Phe  
 233 <210> SEQ ID NO: 8

The 213 response Artificial  
 Sequence requires an explanation  
 in field 223. Peptide is not  
 a sufficient description

*may*  
 The type of errors shown exist throughout  
 the Sequence Listing. Please check subsequent  
 sequences for similar errors.



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Input Set : A:\A-690.ST25.txt

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315 <221> NAME/KEY: misc\_feature  
316 <222> LOCATION: (1)..(1)  
317 <223> OTHER INFORMATION: Attached by optional linker to Fc domain at the N-terminus.  
321 <220> FEATURE:  
322 <221> NAME/KEY: misc\_feature  
323 <222> LOCATION: (18)..(18)  
324 <223> OTHER INFORMATION: Attached by optional linker to an identical sequence  
327 <400> SEQUENCE: 11  
329 Asp Trp Leu Lys Ala Phe Tyr Asp Lys Val Ala Glu Lys Leu Lys Glu  
330 1                   5                   10                   15  
333 Ala Phe

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/09/840,669

DATE: 08/27/2001

TIME: 15:10:38

Input Set : A:\A-690.ST25.txt

Output Set: N:\CRF3\08272001\I840669.raw